RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10 507,343

Source: PCT

Date Processed by STIC: 4-28-05

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PCT

RAW SEQUENCE LISTING   DATE: 04/28/2005
PATENT APPLICATION: **US/10/507,343**   TIME: 16:23:13

Input Set : **E:\405uspc.app.txt**
Output Set: **N:\CRF4\04272005\J507343.raw**

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 3 <110> APPLICANT: Ema, Hideo
 4        Nakauchi, Hiromitsu
 5        Osawa, Mitsujiro
 7 <120> TITLE OF INVENTION: PROTEIN SUSTAINING UNDIFFERENTIATED STEM CELLS
 9 <130> FILE REFERENCE: 790086.405USPC
11 <140> CURRENT APPLICATION NUMBER: US 10/507,343
12 <141> CURRENT FILING DATE: 2004-09-10
14 <150> PRIOR APPLICATION NUMBER: PCT/JP02/02265
15 <151> PRIOR FILING DATE: 2002-03-11
17 <160> NUMBER OF SEQ ID NOS: 27
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1140
23 <212> TYPE: DNA
24 <213> ORGANISM: Mus musculus
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29 gacgcccatc aggctagagt gctcatagga tttgaagaag acattctgat tgtctcggag 180
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40 aaatgtattt gccctcctgg actcgaggga gagcagtgtg aactcagcaa atgcccccaa 840
41 ccctgccgaa atggaggtaa atgcattggt aaaagcaagt gtaagtgccc gaaaggttac 900
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43 cacgaaccca acaagtgcca gtgtcgagag ggctggcacg gcagacactg caataagagg 1020
44 tatggagcca gcctcatgca tgccccgagg ccagcaggcg ccgggctgga gcgacacacg 1080
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64        50                  55                  60
66 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
67  65                  70                  75                  80
69 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
70                  85                  90                  95
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85                 165                 170                 175
87 Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
88           180                 185                 190
90 Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
91        195                 200                 205
93 Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
94        210                 215                 220
96 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
97 225                 230                 235                 240
99 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
100                245                 250                 255
102 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
103           260                 265                 270
105 Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
106        275                 280                 285
108 Ile Gly Lys Ser Lys Cys Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu
109     290                 295                 300
111 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
112 305                 310                 315                 320
114 His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly Arg His
115                325                 330                 335
117 Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg Pro Ala
118        340                 345                 350
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124     370                 375
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128 <211> LENGTH: 1140
129 <212> TYPE: DNA
130 <213> ORGANISM: Homo sapiens
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135 gatgctcacc aggcaagagt actcatagga tttgaagaag atatcctgat tgtttcagag 180
136 gggaaaatgg cacctttttac acatgatttc agaaaagcgc aacagagaat gccagctatt 240
137 cctgtcaata tccattccat gaattttacc tggcaagctg cagggcaggc agaatacttc 300
138 tatgaattcc tgtccttgcg ctccctggat aaaggcatca tggcagatcc aaccgtcaat 360
139 gtccctctgc tgggaacagt gcctcacaag gcatcagttg ttcaagttgg tttcccatgt 420
140 cttggaaaac aggatggggt ggcagcattt gaagtggatg tgattgttat gaattctgaa 480
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144 ggtggacttt gtgtgactcc tggtttctgc atctgcccac ctggattcta tggagtgaac 720
145 tgtgacaaag caaactgctc aaccacctgc tttaatggag ggacctgttt ctaccctgga 780
146 aaatgtattt gccctccagg actagaggga gagcagtgtg aaatcagcaa atgcccacaa 840
147 ccctgtcgaa atggaggtaa atgcattggt aaaagcaaat gtaagtgttc caaaggttac 900
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149 catgaaccca caaatgccca atgtcaagaa ggttggcatg gaagacactg caataaaagg 1020
150 tacgaagcca gcctcataca tgccctgagg ccagcaggcg cccagctcag gcagcacacg 1080
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155 <211> LENGTH: 379
156 <212> TYPE: PRT
157 <213> ORGANISM: Homo sapiens
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163 Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln
164             20                  25                  30
166 Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
167         35                  40                  45
169 Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
170       50                  55                  60
172 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
173 65                  70                  75                  80
175 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
176             85                  90                  95
178 Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
179             100                 105                 110
181 Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
182         115                 120                 125
184 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
185       130                 135                 140
187 Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu
188 145                 150                 155                 160
190 Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
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193 Cys Leu Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
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199 Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys
200     210             215                 220
202 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
203 225                 230                 235                 240
205 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
206             245                 250                 255
208 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
209             260             265                 270
211 Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
212         275             280                 285
214 Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu
215     290             295                 300
217 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
218 305                 310                 315                 320
220 His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His
221             325                 330                 335
223 Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala
224         340                 345                 350
226 Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu
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241 gacgcccatc aggccagagt actcatagga tttgaagaag atattctgat tgtctcggag 180
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243 cccgtcaata tccactccat gaattttacc tggcaagctt cagggcaggc agagtacttc 300
244 tatgagttcc tgtcgctgcg ctcgctggat aaaggcatca tggcagaccc aactgtcaat 360
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253 ccctgccgaa acggaggtaa atgcattggt aaaagcaagt ctgtctgcga gcctggctgc 900
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255 agacactgca ataaaaggta cggagccagc ctcatgcatg ccccgaggcc agcaggcgcc 1020
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270             20                  25                  30
272 Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
273         35                  40                  45
275 Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
276     50                  55                  60
278 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
279 65                  70                  75                  80
281 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ser Gly Gln
282                 85                  90                  95
284 Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
285             100                 105                 110
287 Ile Met Ala Asp Pro Thr Val Asn Val Pro Arg Leu Gly Thr Val Pro
288         115                 120                 125
290 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
291     130                 135                 140
293 Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
294 145                 150                 155                 160
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297             165                 170                 175
299 Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
300         180                 185                 190
302 Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
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306     210                 215                 220
308 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
309 225                 230                 235                 240
311 Cys Asp Lys Ala Asn Cys Ser Ala Thr Cys Phe Asn Gly Gly Thr Cys
312             245                 250                 255
314 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
315             260                 265                 270
317 Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
318         275                 280                 285
320 Ile Gly Lys Ser Lys Ser Val Cys Glu Pro Gly Cys Gly Ala His Gly
321     290                 295                 300
323 Thr Cys His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly
324 305                 310                 315                 320
326 Arg His Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg
327             325                 330                 335
329 Pro Ala Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala
330             340                 345                 350
332 Glu Gly Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/28/2005
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Input Set : E:\405uspc.app.txt
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:12; N Pos. 4,7,10,16,22
Seq#:26; Xaa Pos. 2,3,4,6,7,8,9,10,12,13,14,15,16,18,20,21,22,23,24,25,26
Seq#:26; Xaa Pos. 27,29,30,31,32
Seq#:27; Xaa Pos. 2,3,4,5,6,7,8,10,11,12,13,15,16,17,18,19,20,21,22,23,24
Seq#:27; Xaa Pos. 26,28,29,30,31,32,33,34,35

VERIFICATION SUMMARY   DATE: 04/28/2005
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Input Set : **E:\405uspc.app.txt**
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L:563 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:575 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:579 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:1288 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1293 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
M:341 Repeated in SeqNo=26
L:1309 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1314 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:27
L:1315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
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